

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
Corley, Neil C.  
Guegler, Karl J.  
Patterson, Chandra  
Baughn, Mariah

(ii) TITLE OF THE INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Dr.  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C.  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PF-0519 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1PLB02  
(B) CLONE: 157658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Ala	Glu	Val	Ile	His	Gln	Val	Glu	Glu	Ala	Leu	Asp	Thr	Asp
1				5				10						15	
Glu	Lys	Glu	Met	Leu	Leu	Phe	Leu	Cys	Arg	Asp	Val	Ala	Ile	Asp	Val
			20					25						30	

Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly  
 35 40 45  
 Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg  
 50 55 60  
 Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu  
 65 70 75 80  
 Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu  
 85 90 95  
 Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu  
 100 105 110  
 Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu  
 115 120 125  
 Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val  
 130 135 140  
 Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His  
 145 150 155 160  
 Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln  
 165 170 175  
 Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys  
 180 185 190  
 Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser  
 195 200 205  
 Lys Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val  
 210 215 220  
 Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro  
 225 230 235 240  
 Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile  
 245 250 255  
 Ile Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr  
 260 265 270  
 Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly  
 275 280 285  
 Ile Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp  
 290 295 300  
 Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser  
 305 310 315 320  
 Val Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile  
 325 330 335  
 Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro  
 340 345 350  
 Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu  
 355 360 365  
 Asp Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu  
 370 375 380  
 Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp  
 385 390 395 400  
 Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser  
 405 410 415  
 His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg  
 420 425 430  
 Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly  
 435 440 445  
 Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr  
 450 455 460  
 Val Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr  
 465 470 475 480

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PLB02

(B) CLONE: 157658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAAATTGCGC	CACTGCACTC	CAGCCTGGGC	CACAGAGCGA	GACTCTGTCT	CAAAAAAGAA	60
GGAAAGAAAG	AAAGAAAAAA	AAAAACACTC	GCAGTGTTTA	CTCCTAACGC	GTGGAACCTG	120
TGTCGACATC	CACCCCCGGT	TACTGCATAC	TCAGTCACAC	AAGCCATAGC	AGGAAACAGC	180
GAGCTTGCAG	CCTCACCGAC	GAGTCTCAAC	TAAAAGGGAC	TCCCGGAGCT	AGGGGTGGGG	240
ACTCGGCCTC	ACACAGTGAG	TGCCGGCTAT	TGGACTTTTG	TCCAGTGACA	GCTGAGACAA	300
CAAGGACCAC	GGGAGGAGGT	GTAGGAGAGA	AGCGCCGCGA	ACAGCGATCG	CCCAGCACCA	360
AGTCCGCTTC	CAGGCTTTTC	GTTTCTTTGC	CTCCATCTTG	GGTGCGCCTT	CCCGGCGTCT	420
AGGGGAGCGA	AGGCTGAGGT	GGCAGCGGCA	GGAGAGTCCG	GCCGCGACAG	GACGAACCTC	480
CCCCTGGAA	AGGATTCTGA	AAGAAATGAA	GTCAGCCCTC	AGAAATGAAG	TTGACTGCCT	540
GCTGGCTTTC	TGTTGACTGG	CCCGGAGCTG	TACTGCAAGA	CCCTTGTGAG	CTTCCCTAGT	600
CTAAGAGTAG	GATGTCTGCT	GAAGTCATCC	ATCAGGTTGA	AGAAGCACTT	GATACAGATG	660
AGAAGGAGAT	GCTGCTCTTT	TTGTGCCGGG	ATGTTGCTAT	AGATGTGGTT	CCACCTAATG	720
TCAGGGACCT	TCTGGATATT	TTACGGGAAA	GAGGTAAGCT	GTCTGTCGGG	GACTTGGCTG	780
AACTGCTCTA	CAGAGTGAGG	CGATTTGACC	TGCTCAAACG	TATCTGAAG	ATGGACAGAA	840
AAGCTGTGGA	GACCCACCTG	CTCAGGAACC	CTCACCTTGT	TTCGGACTAT	AGAGTGCTGA	900
TGGCAGAGAT	TGGTGAGGAT	TTGGATAAAT	CTGATGTGTC	CTCATTAATT	TTCCCTCATGA	960
AGGATTACAT	GGGCCGAGGC	AAGATAAGCA	AGGAGAAGAG	TTTCTTGGAC	CTTGTGGTTG	1020
AGTTGGAGAA	ACTAAATCTG	GTTGCCCCAG	ATCAACTGGA	TTTATTAGAA	AAATGCCTAA	1080
AGAACATCCA	CAGAATAGAC	CTGAAGACAA	AAATCCAGAA	GTACAAGCAG	TCTGTTCAAG	1140
GAGCAGGGAC	AAGTTACAGG	AATGTTCTCC	AAGCAGCAAT	CCAAAAGAGT	CTCAAGGATC	1200
CTTCAAATAA	CTTCAGGCTC	CATAATGGGA	GAAGTAAAGA	ACAAAGACTT	AAGGAACAGC	1260
TTGGCGCTCA	ACAAGAACCA	GTGAAGAAAT	CCATTCAAGG	ATCAGAAGCT	TTTTTGCCTC	1320
AGAGCATACC	TGAAGAGAGA	TACAAGATGA	AGAGCAAGCC	CCTAGGAATC	TGCCGTGATAA	1380
TCGATTGCAT	TGGCAATGAG	ACAGAGCTTC	TTCGAGACAC	CTTCACTTCC	CTGGGCTATG	1440
AAGTCCAGAA	ATTCTTGCAT	CTCAGTATGC	ATGGTATATC	CCAGATTCTT	GGCCAATTTG	1500
CCTGTATGCC	CGAGCACCGA	GACTACGACA	GCTTTGTGTG	TGTCCTGGTG	AGCCGAGGAG	1560
GCTCCCAGAG	TGTGTATGGT	GTGGATCAGA	CTCACTCCGG	GCTCCCCCTG	CATCACATCA	1620
GGAGGATGTT	CATGGGAGAT	TCATGCCCTT	ATCTAGCAGG	GAAGCCAAAG	ATGTTTTTTTA	1680
TTCAGAACTA	TGTGGTGTCA	GAGGGCCAGC	TGGAGGACAG	CAGCCTCTTG	GAGGTGGATG	1740
GGCCAGCGAT	GAAGAATGTG	GAATTCAAGG	CTCAGAAGCG	AGGGCTGTGC	ACAGTTCACC	1800
GAGAAGCTGA	CTTCTTCTGG	AGCCTGTGTA	CTGCGGACAT	GTCCCTGCTG	GAGCAGTCTC	1860
ACAGCTCACC	ATCCCTGTAC	CTGCAGTGCC	TCTCCCAGAA	ACTGAGACAA	GAAAGAAAAC	1920
GCCCCTCCT	GGATCTTCAC	ATTGAACTCA	ATGGCTACAT	GTATGATTGG	AACAGCAGAG	1980
TTTCTGCCAA	GGAGAAATAT	TATGTCTGGC	TGCAGCACAC	TCTGAGAAAG	AAACTTATCC	2040
TCTCCTACAC	ATAAGAAACC	AAAAGGCTGG	GCGTAGTGCC	TCACACCTGT	GATCCCAGCA	2100
CTTTGGGAGG	CCAAGGAGGG	CAGATCACTT	CAGGTCAGGA	GTTTCGAGACC	AGCCTGGCCA	2160
ACATGGTAAA	CGCTGTCCCT	AGTAAAAATA	CAAAAATTAG	CTGGGTGTGG	GTGTGGGTAC	2220
CTGTATTCCC	AGTTACTTGG	GAGGCTGAGG	TGGGAGGATC	TTTTGAACCC	AGGAGTTCAG	2280
GGTCATAGCA	TGCTGTGATT	GTGCCTACGA	ATAGCCACTG	CATACCAACC	TGGGCAATAT	2340
AGCAAGATCC	CA					2352

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 642272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Glu	Tyr	Ala	Met	Lys	Ser	Leu	Ser	Leu	Leu	Tyr	Pro	Lys	Ser	Leu
1				5					10					15	
Ser	Arg	His	Val	Ser	Val	Arg	Thr	Ser	Val	Val	Thr	Gln	Gln	Leu	Leu
			20					25					30		
Ser	Glu	Pro	Ser	Pro	Lys	Ala	Pro	Arg	Ala	Arg	Pro	Cys	Arg	Val	Ser
		35					40				45				
Thr	Ala	Asp	Arg	Ser	Val	Arg	Lys	Gly	Ile	Met	Ala	Tyr	Ser	Leu	Glu
	50					55				60					

Asp Leu Leu Leu Lys Val Arg Asp Thr Leu Met Leu Ala Asp Lys Pro  
 65 70 75 80  
 Phe Phe Leu Val Leu Glu Glu Asp Gly Thr Thr Val Glu Thr Glu Glu  
 85 90 95  
 Tyr Phe Gln Ala Leu Ala Gly Asp Thr Val Phe Met Val Leu Gln Lys  
 100 105 110  
 Gly Gln Lys Trp Gln Pro Pro Ser Glu Gln Gly Thr Arg His Pro Leu  
 115 120 125  
 Ser Leu Ser His Lys Pro Ala Lys Lys Ile Asp Val Ala Arg Val Thr  
 130 135 140  
 Phe Asp Leu Tyr Lys Leu Asn Pro Gln Asp Phe Ile Gly Cys Leu Asn  
 145 150 155 160  
 Val Lys Ala Thr Phe Tyr Asp Thr Tyr Ser Leu Ser Tyr Asp Leu His  
 165 170 175  
 Cys Cys Gly Ala Lys Arg Ile Met Lys Glu Ala Phe Arg Trp Ala Leu  
 180 185 190  
 Phe Ser Met Gln Ala Thr Gly His Val Leu Leu Gly Thr Ser Cys Tyr  
 195 200 205  
 Leu Gln Gln Leu Leu Asp Ala Thr Glu Glu Gly Gln Pro Pro Lys Gly  
 210 215 220  
 Lys Ala Ser Ser Leu Ile Pro Thr Cys Leu Lys Ile Leu Gln  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03  
 (B) CLONE: 642272

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATGTTCTTT	TGGCCACTGT	GAAGCCTCAG	GAAGGGGCTC	GGATTGCTCA	AGGACCCATG	60
GGAGAGAGGA	GGCTTTGACT	GGGCTGCCTG	CCTGTGAGGT	CTCTGGACTA	GAGGTCCAAC	120
GCAGTCCAGC	TGACAAGGAT	GGAATACGCC	ATGAAGTCCC	TTAGCCTTCT	CTACCCCAAG	180
TCCCTCTCCA	GGCATGTGTC	AGTGCGTACC	TCTGTGGTGA	CCCAGCAGCT	GCTGTCGGAG	240
CCCAGCCCCA	AGGCCCCAG	GGCCCGGCC	TGCCGCGTAA	GCACGGCGGA	TCGAAGCGTG	300
AGGAAGGGCA	TCATGGCTTA	CAGTCTTGAG	GACCTCCTCC	TCAAGGTCCG	GGACACTCTG	360
ATGCTGGCAG	ACAAGCCCTT	CTTCCTGGTG	CTGGAGGAAG	ATGGCACAAAC	TGTAGAGACA	420
GAAGAGTACT	TCCAAGCCCT	GGCAGGGGAT	ACAGTGTTC	TGGTCCTCCA	GAAGGGGCAG	480
AAATGGCAGC	CCCCATCAGA	ACAGGGGACA	AGGCACCCAC	TGTCCCTCTC	CCATAAGCCT	540
GCCAAGAAGA	TTGATGTGGC	CCGTGTAACG	TTTGATCTGT	ACAAGCTGAA	CCCACAGGAC	600
TTCATTGGCT	GCCTGAACGT	GAAGGCGACT	TTTTATGATA	CATACTCCCT	TTCTTATGAT	660
CTGCACTGCT	GTGGGGCCAA	GCGCATCATG	AAGGAAGCTT	TCCGCTGGGC	CCTCTTCAGC	720
ATGCAGGCCA	CAGGCCACGT	ACTGCTTGGC	ACCTCCTGTT	ACCTGCAGCA	GCTCCTCGAT	780
GCTACGGAGG	AAGGGCAGCC	CCCCAAGGGC	AAGGCCTCAT	CCCTTATCCC	GACCTGTCTG	840
AAGATACTGC	AGTGAAAGCC	CAAGTCCTTG	GAAGCTTTCC	CCAGTGAAGG	ACTGACTGGG	900
GGCCTCACGC	TTAACTGGTA	GTGCCCACAA	GCCTGGCAGC	TGTAGAGCCG	CGAACCTCCC	960
CACACCTCCC	TCACCGCGCA	GGACCCTGAG	TGAGGAGGAG	GAGCTGGAAA	CCTGGGGTGG	1020
GTTGGCCAAA	GGAGAACCTC	AAGCTCCTGG	CCTGATCCAG	CTCCTTCCTG	CCCAAGGCAG	1080
CTTAGCCCAT	CCAGACTGGT	CCTGAAGTCT	GTCCCTCCAT	TGGCATGAAG	TCTGCCCTTT	1140
AGCAATCCGG	CCTCGCAGGC	TGTACTTTCA	TGGTGCTCTC	TACCTTCTGG	CCCCCATCCC	1200
GGAACATTCC	TGAGTGAATT	CGCAAGCGCA	CTAGCATGTG	ATATTAGGGA	GTTTGCAATA	1260
AATTATTGAG	GCTGAAAAAA	AAAA				1284

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: PENITUT01  
 (B) CLONE: 1453807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Gln	Glu	Gln	Val	Ser	Glu	Tyr	Leu	Gly	Val	Thr	Ser	Phe	Lys	1	5	10	15
Arg	Lys	Tyr	Pro	Asp	Leu	Glu	Arg	Arg	Asp	Leu	Ser	His	Lys	Glu	Lys	20	25	30	
Leu	Tyr	Leu	Arg	Glu	Leu	Asn	Val	Ile	Thr	Glu	Thr	Gln	Cys	Thr	Leu	35	40	45	
Gly	Leu	Thr	Ala	Leu	Arg	Ser	Asp	Glu	Val	Ile	Asp	Leu	Met	Ile	Lys	50	55	60	
Glu	Tyr	Pro	Ala	Lys	His	Ala	Glu	Tyr	Ser	Val	Ile	Leu	Gln	Glu	Lys	65	70	75	80
Glu	Arg	Gln	Arg	Ile	Thr	Asp	His	Tyr	Lys	Glu	Tyr	Ser	Gln	Met	Gln	85	90	95	
Gln	Gln	Asn	Thr	Gln	Lys	Val	Glu	Ala	Ser	Lys	Val	Pro	Glu	Tyr	Ile	100	105	110	
Lys	Lys	Ala	Ala	Lys	Lys	Ala	Ala	Glu	Phe	Asn	Ser	Asn	Leu	Asn	Arg	115	120	125	
Glu	Arg	Met	Glu	Glu	Arg	Arg	Ala	Tyr	Phe	Asp	Leu	Gln	Thr	His	Val	130	135	140	
Ile	Gln	Val	Pro	Gln	Gly	Lys	Tyr	Lys	Val	Leu	Pro	Thr	Glu	Arg	Thr	145	150	155	160
Lys	Val	Ser	Ser	Tyr	Pro	Val	Ala	Leu	Ile	Pro	Gly	Gln	Phe	Gln	Glu	165	170	175	
Tyr	Tyr	Lys	Arg	Tyr	Ser	Pro	Asp	Glu	Leu	Arg	Tyr	Leu	Pro	Leu	Asn	180	185	190	
Thr	Ala	Leu	Tyr	Glu	Pro	Pro	Leu	Asp	Pro	Glu	Leu	Pro	Ala	Leu	Asp	195	200	205	
Ser	Asp	Gly	Asp	Ser	Asp	Asp	Gly	Glu	Asp	Gly	Arg	Gly	Asp	Glu	Lys	210	215	220	
Arg	Lys	Asn	Lys	Gly	Thr	Ser	Asp	Ser	Ser	Ser	Gly	Asn	Val	Ser	Glu	225	230	235	240
Gly	Glu	Ser	Pro	Pro	Asp	Ser	Gln	Glu	Asp	Ser	Phe	Gln	Gly	Arg	Gln	245	250	255	
Lys	Ser	Lys	Asp	Lys	Ala	Ala	Thr	Pro	Arg	Lys	Asp	Gly	Pro	Lys	Arg	260	265	270	
Ser	Val	Leu	Ser	Lys	Ser	Val	Pro	Gly	Tyr	Lys	Pro	Lys	Val	Ile	Pro	275	280	285	
Asn	Ala	Ile	Cys	Gly	Ile	Cys	Leu	Lys	Gly	Lys	Glu	Ser	Asn	Lys	Lys	290	295	300	
Gly	Lys	Ala	Glu	Ser	Leu	Ile	His	Cys	Ser	Gln	Cys	Glu	Asn	Ser	Gly	305	310	315	320
His	Pro	Ser	Cys	Leu	Asp	Met	Thr	Met	Glu	Leu	Val	Ser	Met	Ile	Lys	325	330	335	
Thr	Tyr	Pro	Trp	Gln	Cys	Met	Glu	Cys	Lys	Thr	Cys	Ile	Ile	Cys	Gly	340	345	350	
Gln	Pro	His	His	Glu	Glu	Glu	Met	Phe	Cys	Asp	Met	Cys	Asp	Arg		355	360	365	
Gly	Tyr	His	Thr	Phe	Cys	Val	Gly	Leu	Gly	Ala	Ile	Pro	Ser	Gly	Arg	370	375	380	
Trp	Ile	Cys	Asp	Cys	Cys	Gln	Arg	Ala	Pro	Pro	Thr	Pro	Arg	Lys	Val	385	390	395	400
Gly	Arg	Arg	Gly	Lys	Asn	Ser	Lys	Glu	Gly							405	410		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: PENITUT01  
 (B) CLONE: 1453807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGGTTTTTA	GTTACTATCC	AGCAGAAAAC	TTGATAGAGT	ACAAATGGCC	ACCTGATGAA	60
ACAGGAGAAT	ACTATATGCT	TCAAGAACAA	GTCAGTGAAT	ATTTGGGTGT	GACCTCCTTT	120
AAAAGGAAAT	ATCCAGATTT	AGAGCGACGA	GATTTGTCTC	ACAAGGAGAA	ACTCTACCTG	180
AGAGAGCTAA	ATGTCATTAC	TGAAACTCAG	TGCACTCTAG	GCTTAACAGC	ATTGCGCAGT	240
GATGAAGTGA	TTGATTTAAT	GATAAAAGAA	TATCCAGCCA	AACATGCTGA	GTATTCTGTT	300
ATTCTACAAG	AAAAAGAACG	TCAACGAATT	ACAGACCATT	ATAAAGAGTA	TTCCCAAATG	360
CAACAACAGA	ATACTCAGAA	AGTTGAAGCC	AGTAAAGTGC	CTGAGTATAT	TAAGAAAGCT	420
GCCAAAAAAG	CAGCAGAATT	TAATAGCAAC	TTAAACCGGG	AACGCATGGA	AGAAAGAAGA	480
GCTTATTTTG	ACTTGCAGAC	ACATGTTATC	CAGGTACCTC	AAGGGAAGTA	CAAAGTTTTG	540
CCAACAGAGC	GAACAAAGGT	CAGTTCTTAC	CCAGTGGCTC	TCATCCCCGG	ACAGTTCCAG	600
GAATATTATA	AGAGGTACTC	ACCAGATGAG	TGCGGGTATC	TGCCATTAAA	CACAGCCCTG	660
TATGAGCCCC	CTCTGGATCC	TGAGCTCCCT	GCTCTAGACA	GTGATGGTGA	TTCAGATGAT	720
GGCGAAGATG	GTCGAGGTGA	TGAGAAACGG	AAAAATAAAG	GCACTTCGGA	CAGCTCCTCT	780
GGCAATGTAT	CTGAAGGGGA	AAGCCCTCCT	GACAGCCAGG	AGGACTCTTT	CCAGGGAAGA	840
CAGAAATCAA	AAGACAAAGC	TGCCACTCCA	AGAAAAGATG	GTCCCAAACG	TTCTGTACTG	900
TCCAAGTCAG	TTCTTGGGTA	CAAGCCAAAG	GTCATTCCAA	ATGCTATATG	TGGAATTTGT	960
CTGAAGGGTA	AGGAGTCCAA	CAAGAAAGGA	AAGGTGAAAT	CACTTATACA	CTGTCCCAA	1020
TGTGAGAATA	GTGGCCATCC	TTCTTGCCTG	GATATGACAA	TGGAGCTTGT	TTCTATGATT	1080
AAGACCTACC	CATGGCAGTG	TATGGAATGT	AAAACATGCA	TTATATGTGG	ACAACCCAC	1140
CATGAAGAAG	AAATGATGTT	CTGTGATATG	TGTGACAGAG	GTTATCATAC	TTTTTGTGTG	1200
GGCCTTGGTG	CTATTCCATC	AGGTCGCTGG	ATTTGTGACT	GTTGTCAGCG	GGCCCCCCCC	1260
ACACCCAGGA	AAGTGGGCAG	AAGGGGGAAA	AACAGCAAAAG	AGGGATAAAA	TAGTTTTTTGA	1320
CTCTAATACT	GTATATGCAT	TTAAGTGGAA	TATTTGGTGC	CATTTACAAC	ATTATTTTCA	1380
TGCCAATAAA	AGATTTTTTT	TGCAAATTAT	GAGCTTAAAA	TCTGCAGTTA	TTTCTGTTAA	1440
AAGTACGCTT	ACTCTCGAAA	CTAACTCCAG	GTAGAGAATT	CATCTTCCAA	AGTATTTTAT	1500
AGTAACCTTG	GCTCACTCCA	AAAATTCAGT	GGAAATGTTT	AGTAACTTAA	GATACTTAAC	1560
TGTTTCTCCA	TAGCCCCAAA	AGTTAATTTT	CATGAACTTT	CCTAATCTAC	ATTGTTTCCG	1620
GCCTACCATA	GGTAGCACTG	ACAAGATTAT	TTAATAACTG	AAGAATTTTC	ATAGGTATGA	1680
CAAAATGGCCC	ACTAAGATTT	GGTGCAGCTG	GATTTAGAGT	TGTCATTATT	GGACTGGTAC	1740
AGGAACAAAC	TTTGTAATAA	CCTGCCTGCC	AGGAAATCCT	TTTTGTATAG	AAAAGTACCA	1800
TCACCTACTT	GGGGTACAGG	CATGAGGCTT	TAGTCCAGGC	TCAGGGAAGT	GTACGTAAAT	1860
CATTTCCAAC	TTGATTTTAG	TAACCTTTGA	AAACTTACAC	CAACTTCGGT	TAGAATCTCC	1920
AGAGTAAAAT	TACAAAGTTA	TCAACCTTTT	GATTTGTGTC	ACAGCATGAA	AGGTTGCTCT	1980
ATTTTATATA	AACCTGTTAC	TGCAATCATT	TTTAGTCAAC	CTGCCAATG	AAATGGAGT	2040
CTAAACACTT	TGTGCACAGT	CCTTTTATAG	GAATTATGAT	CTTTAAAATA	CTGTGCTTGC	2100
TGCTTTTCCT	ATTTTGGGG	TAAGTGAAGT	AACAAAATGC	GTATGGCTTT		2150

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: OVARNOT03  
 (B) CLONE: 2059022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Asn	Ser	Gly	Leu	Gln	Leu	Leu	Gly	Phe	Ser	Met	Ala	Leu	Leu
1				5					10					15	
Gly	Trp	Val	Gly	Leu	Val	Ala	Cys	Thr	Ala	Ile	Pro	Gln	Trp	Gln	Met
			20					25					30		
Ser	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Ile	Thr	Ala	Gln	Ala	Met	Tyr	Lys
		35				40					45				
Gly	Leu	Trp	Met	Asp	Cys	Val	Thr	Gln	Ser	Thr	Gly	Met	Met	Ser	Cys
	50					55					60				
Lys	Met	Tyr	Asp	Ser	Val	Leu	Ala	Leu	Ser	Ala	Ala	Leu	Gln	Ala	Thr
65					70					75				80	

Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe  
                             85                            90                            95  
 Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys  
                             100                            105                            110  
 Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe Ile Val  
                             115                            120                            125  
 Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr Gly His Gln Ile  
                             130                            135                            140  
 Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu  
                             145                            150                            155                            160  
 Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu Val Ile  
                             165                            170                            175  
 Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys  
                             180                            185                            190  
 Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser Ser Lys  
                             195                            200                            205  
 Glu Tyr Val  
                             210

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARNOT03  
 (B) CLONE: 2059022

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCCACGCGTC	CGCTCACCTC	CGAGCCACCT	CTGCTGCGCA	CCGCAGCCTC	GGACCTACAG	60
CCCAGGATAC	TTTGGGACTT	GCCGGCGCTC	AGAAACGCGC	CCAGACGGCC	CCTCCACCTT	120
TTGTTTGCCT	AGGGTCGCCG	AGAGCGCCCG	GAGGGAACCG	CCTGGCCTTC	GGGGACCACC	180
AATTTTGTCT	GGAACCACCC	TCCCGGCGTA	TCCTACTCCC	TGTGCCGCGA	GGCCATCGCT	240
TCACTGGAGG	GGTCGATTGT	TGTGTAGTTT	GGTGACAAGA	TTTGCATTC	CCTGGCCCAA	300
ACCCTTTTGT	TCTCTTTGGG	TGACCGGAAA	ACTCCACCTC	AAGTTTCTT	TTGTGGGGCT	360
GCCCCCAAG	TGTCGTTTGT	TTTACTGTAG	GGTCTCCCCG	CCCGGCGCCC	CCAGTGTTTT	420
CTGAGGGCGG	AAATGGCCAA	TTCGGGCCTG	CAGTTGCTGG	GCTTCTCCAT	GGCCCTGCTG	480
GGCTGGGTGG	GTCTGGTGGC	CTGCACCGCC	ATCCCGCAGT	GGCAGATGAG	CTCCTATGCG	540
GGTGACAACA	TCATCACGGC	CCAGGCCATG	TACAAGGGGC	TGTGGATGGA	CTGCGTCACG	600
CAGAGCACGG	GGATGATGAG	CTGCAAAATG	TACGACTCGG	TGCTCGCCCT	GTCCGCGGCC	660
TTGCAGGCCA	CTCGAGCCCT	AATGGTGGTC	TCCCTGGTGC	TGGGCTTCCT	GGCCATGTTT	720
GTGGCCACGA	TGGGCATGAA	GTGCACGGCG	TGTGGGGGAG	ACGACAAAGT	GAAGAAGGCC	780
CGTATAGCCA	TGGGTGGAGG	CATAATTTTC	ATCGTGGCAG	GTCTTGCCGC	CTTGGTAGCT	840
TGCTCCTGGT	ATGGCCATCA	GATTGTGACA	GACTTTTATA	ACCCTTTGAT	CCCTACCAAC	900
ATTAAGTATG	AGTTTGGCCC	TGCCATCTTT	ATTGGCTGGG	CAGGGTCTGC	CCTAGTCATC	960
CTGGGAGGTG	CACTGCTCTC	CTGTTCTCTG	CCTGGGAATG	AGAGCAAGGC	TGGGTACCGT	1020
GCACCCCGCT	CTTACCCTAA	GTCCAACTCT	TCCAAGGAGT	ATGTGTGACC	TGGGATCTCC	1080
TTGCCCCAGC	CTGACAGGCT	ATGGGAGTGT	CTAGATGCCT	GAAAGGGCCT	GGGGCTGAGC	1140
TCAGCCTGTG	GGCAGGGTGC	CGGACAAAGG	CCTCCTGGTC	ACTCTGTCCC	TGCACTCCAT	1200
GTATAGTCCT	CTTGGGTTGG	GGGTGGGGGG	GTGCCGTTGG	TGGGAGAGAC	AAAAAGAGGG	1260
AGAGTGTGCT	TTTTGTACAG	TAATAAAAAA	TAAGTATTGG	GAAGCAGGCT	TTTTTCCCTT	1320
CAGGGCCTCT	GCTTTCCTCC	CGTCCAGATC	CTTGCAGGGA	GCTTGGAACC	TTAGTGCACC	1380
TACTTCAGTT	CAGAACACTT	AGCACCCAC	TGACTCCACT	GACAATTGAC	TAAAAGATGC	1440
AGGTGCTCGT	ATCTCGACAT	TCATTCCCAC	CCCCCTCTTA	TTTAAATAGC	TACCAAAGTA	1500
CTTCTTTTTT	AATAAAAAAA	TAAAGATTTT	TATTAAAAAA	AAAAAA		1546

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: Swiss-Prot  
 (B) CLONE: p56198

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Asp Tyr Ala Met Lys Ser Leu Ser Leu Leu Tyr Pro Arg Ser Leu
1      5      10      15
Ser Arg His Val Ala Val Ser Thr Ala Val Val Thr Gln Gln Leu Val
20     25     30
Ser Lys Pro Ser Arg Glu Thr Pro Arg Ala Arg Pro Cys Arg Val Ser
35     40     45
Thr Ala Asp Arg Lys Val Arg Lys Gly Ile Met Ala His Ser Leu Glu
50     55     60
Asp Leu Leu Asn Lys Val Gln Asp Ile Leu Lys Leu Lys Asp Lys Pro
65     70     75     80
Phe Ser Leu Val Leu Glu Glu Asp Gly Thr Ile Val Glu Thr Glu Glu
85     90     95
Tyr Phe Gln Ala Leu Ala Lys Asp Thr Met Phe Met Val Leu Leu Lys
100    105    110
Gly Gln Lys Trp Lys Pro Pro Ser Glu Gln Arg Lys Lys Arg Ala Gln
115    120    125
Leu Ala Leu Ser Gln Lys Pro Thr Lys Lys Ile Asp Val Ala Arg Val
130    135    140
Thr Phe Asp Leu Tyr Lys Leu Asn Pro Gln Asp Phe Ile Gly Cys Leu
145    150    155    160
Asn Val Lys Ala Thr Leu Tyr Asp Thr Tyr Ser Leu Ser Tyr Asp Leu
165    170    175
His Cys Tyr Lys Ala Lys Arg Ile Val Lys Glu Ile Val Arg Trp Thr
180    185    190
Leu Phe Ser Met Gln Ala Thr Gly His Met Leu Leu Gly Thr Ser Ser
195    200    205
Tyr Met Gln Gln Phe Leu Asp Ala Thr Glu Glu Glu Gln Pro Ala Lys
210    215    220
Ala Lys Pro Ser Ser Leu Leu Pro Ala Cys Leu Lys Met Leu Gln
225    230    235

```

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 2065561

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Glu Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg
1      5      10      15
Thr Leu Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His
20     25     30
Gly Val Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp
35     40     45
Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala
50     55     60
Glu Asp Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro
65     70     75     80
Ser Asn Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr
85     90     95
Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp
100    105    110
Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala
115    120    125

```



```

Arg Gln Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu
130          135          140
Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu
145          150          155          160
Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln
          165          170          175
Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu
          180          185          190
Gln Leu Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys
          195          200          205
Gln Glu Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp
          210          215          220
Thr Gly Ile Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His
225          230          235          240
Ile Leu Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser
          245          250          255
Ser Gln Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala
          260          265          270
Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala
          275          280          285
Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His
          290          295          300
Ser Leu Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu
305          310          315          320
Gln Asn Pro Lys Arg Ala Arg Gln Asp Pro Thr
          325          330

```

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 606661

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Glu Gln Cys His Asn Tyr Asn Ala Arg Leu Cys Ala Glu Arg Ser
1          5          10          15
Val Arg Leu Pro Phe Leu Asp Ser Gln Thr Gly Val Ala Gln Ser Asn
          20          25          30
Cys Tyr Ile Trp Met Glu Lys Arg His Arg Gly Pro Gly Leu Ala Ser
          35          40          45
Gly Gln Leu Tyr Ser Tyr Pro Ala Arg Arg Trp Arg Lys Lys Arg Arg
          50          55          60
Ala His Pro Pro Glu Asp Pro Arg Leu Ser Phe Pro Ser Ile Lys Pro
65          70          75          80
Asp Thr Asp Gln Thr Leu Lys Lys Glu Gly Leu Ile Ser Gln Asp Gly
          85          90          95
Ser Ser Leu Glu Ala Leu Leu Arg Thr Asp Pro Leu Glu Lys Arg Gly
          100          105          110
Ala Pro Asp Pro Arg Val Asp Asp Asp Ser Leu Gly Glu Phe Pro Val
          115          120          125
Ser Asn Ser Arg Ala Arg Lys Arg Ile Ile Glu Pro Asp Asp Phe Leu
          130          135          140
Asp Asp Leu Asp Asp Glu Asp Tyr Glu Glu Asp Arg Pro Lys Arg Arg
145          150          155          160
Gly Lys Gly Lys Ser Lys Ser Lys Gly Val Ser Ser Ala Arg Lys Lys
          165          170          175
Leu Asp Ala Ser Ile Leu Glu Asp Arg Asp Lys Pro Tyr Ala Cys Asp
          180          185          190
Ile Cys Gly Lys Arg Tyr Lys Asn Arg Pro Gly Leu Ser Tyr His Tyr
          195          200          205

```

Ala His Ser His Leu Ala Glu Glu Glu Gly Glu Asp Lys Glu Asp Ser  
 210 215 220  
 Arg Pro Pro Thr Pro Val Ser Gln Arg Ser Glu Glu Gln Lys Ser Lys  
 225 230 235 240  
 Lys Gly Pro Asp Gly Leu Ala Leu Pro Asn Asn Tyr Cys Asp Phe Cys  
 245 250 255  
 Leu Gly Asp Ser Lys Ile Asn Lys Lys Thr Gly Gln Pro Glu Glu Leu  
 260 265 270  
 Val Ser Cys Ser Asp Cys Gly Arg Ser Gly His Pro Ser Cys Leu Gln  
 275 280 285  
 Phe Thr Pro Val Met Met Ala Ala Val Lys Thr Tyr Arg Trp Gln Cys  
 290 295 300  
 Ile Glu Cys Lys Cys Cys Asn Leu Cys Gly Thr Ser Glu Asn Asp Asp  
 305 310 315 320  
 Gln Leu Leu Phe Cys Asp Asp Cys Asp Arg Gly Tyr His Met Tyr Cys  
 325 330 335  
 Leu Thr Pro Ser Met Ser Glu Pro Pro Glu Gly Ser Trp Ser Cys His  
 340 345 350  
 Leu Cys Leu Asp Leu Leu Lys Glu Lys Ala Ser Ile Tyr Gln Asn Gln  
 355 360 365  
 Asn Ser Ser  
 370

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 2570129

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly  
 1 5 10 15  
 Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser  
 20 25 30  
 Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly  
 35 40 45  
 Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys  
 50 55 60  
 Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg  
 65 70 75 80  
 Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val  
 85 90 95  
 Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala  
 100 105 110  
 Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala  
 115 120 125  
 Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg  
 130 135 140  
 Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly  
 145 150 155 160  
 Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Leu Gln Leu Leu Gly  
 165 170 175  
 Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr  
 180 185 190  
 Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala  
 195 200 205  
 Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Tyr Val  
 210 215 220